

02/07



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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/977,577

DATE: 02/08/2002  
TIME: 13:59:40

Input Set : A:\MOESTRUP1A.txt  
Output Set: N:\CRF3\02082002\I977577.raw

3 <110> APPLICANT: MOESTRUP, Soren  
4 MOLLER, Holger J.  
6 <120> TITLE OF INVENTION: THE FUNCTION OF A HAPTOGLOBIN-HAEMOGLOBIN RECEPTOR AND THE  
USES THEREOF

8 <130> FILE REFERENCE: MOESTRUP=1A  
10 <140> CURRENT APPLICATION NUMBER: 09/977,577  
11 <141> CURRENT FILING DATE: 2001-10-16  
13 <150> PRIOR APPLICATION NUMBER: US 60/270,120  
14 <151> PRIOR FILING DATE: 2001-02-22  
16 <150> PRIOR APPLICATION NUMBER: DK PA 2001 00039  
17 <151> PRIOR FILING DATE: 2001-01-11  
19 <150> PRIOR APPLICATION NUMBER: DK PA 2000 01543  
20 <151> PRIOR FILING DATE: 2000-10-16  
22 <160> NUMBER OF SEQ ID NOS: 25  
24 <170> SOFTWARE: PatentIn version 3.1  
26 <210> SEQ ID NO: 1  
27 <211> LENGTH: 347  
28 <212> TYPE: PRT  
29 <213> ORGANISM: Homo sapiens  
31 <400> SEQUENCE: 1

33 Met Ser Ala Leu Gly Ala Val Ile Ala Leu Leu Leu Trp Gly Gln Leu  
34 1 5 10 15  
37 Phe Ala Val Asp Ser Gly Asn Asp Val Thr Asp Ile Ala Asp Asp Gly  
38 20 25 30  
41 Cys Pro Lys Pro Pro Glu Ile Ala His Gly Tyr Val Glu His Ser Val  
42 35 40 45  
45 Arg Tyr Gln Cys Lys Asn Tyr Tyr Lys Leu Arg Thr Glu Gly Asp Gly  
46 50 55 60  
49 Val Tyr Thr Leu Asn Asn Glu Lys Gln Trp Ile Asn Lys Ala Val Gly  
50 65 70 75 80  
53 Asp Lys Leu Pro Glu Cys Glu Ala Val Cys Gly Lys Pro Lys Asn Pro  
54 85 90 95  
57 Ala Asn Pro Val Gln Arg Ile Leu Gly Gly His Leu Asp Ala Lys Gly  
58 100 105 110  
61 Ser Phe Pro Trp Gln Ala Lys Met Val Ser His His Asn Leu Thr Thr  
62 115 120 125  
65 Gly Ala Thr Leu Ile Asn Glu Gln Trp Leu Leu Thr Thr Ala Lys Asn  
66 130 135 140  
69 Leu Phe Leu Asn His Ser Glu Asn Ala Thr Ala Lys Asp Ile Ala Pro  
70 145 150 155 160  
73 Thr Leu Thr Leu Tyr Val Gly Lys Lys Gln Leu Val Glu Ile Glu Lys  
74 165 170 175  
77 Val Val Leu His Pro Asn Tyr Ser Gln Val Asp Ile Gly Leu Ile Lys  
78 180 185 190

ENTERED

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81 Leu Lys Gln Lys Val Ser Val Asn Glu Arg Val Met Pro Ile Cys Leu
82      195          200          205
85 Pro Ser Lys Asp Tyr Ala Glu Val Gly Arg Val Gly Tyr Val Ser Gly
86      210          215          220
89 Trp Gly Arg Asn Ala Asn Phe Lys Phe Thr Asp His Leu Lys Tyr Val
90 225          230          235          240
93 Met Leu Pro Val Ala Asp Gln Asp Gln Cys Ile Arg His Tyr Glu Gly
94          245          250          255
97 Ser Thr Val Pro Glu Lys Lys Thr Pro Lys Ser Pro Val Gly Val Gln
98          260          265          270
101 Pro Ile Leu Asn Glu His Thr Phe Cys Ala Gly Met Ser Lys Tyr Gln
102          275          280          285
105 Glu Asp Thr Cys Tyr Gly Asp Ala Gly Ser Ala Phe Ala Val His Asp
106          290          295          300
109 Leu Glu Glu Asp Thr Trp Tyr Ala Thr Gly Ile Leu Ser Phe Asp Lys
110 305          310          315          320
113 Ser Cys Ala Val Ala Glu Tyr Gly Val Tyr Val Lys Val Thr Ser Ile
114          325          330          335
117 Gln Asp Trp Val Gln Lys Thr Ile Ala Glu Asn
118          340          345
121 <210> SEQ ID NO: 2
122 <211> LENGTH: 406
123 <212> TYPE: PRT
124 <213> ORGANISM: Homo sapiens
126 <400> SEQUENCE: 2
128 Met Ser Ala Leu Gly Ala Val Ile Ala Leu Leu Trp Gly Gln Leu
129 1          5          10          15
132 Phe Ala Val Asp Ser Gly Asn Asp Val Thr Asp Ile Ala Asp Asp Gly
133          20          25          30
136 Cys Pro Lys Pro Pro Glu Ile Ala His Gly Tyr Val Glu His Ser Val
137          35          40          45
140 Arg Tyr Gln Cys Lys Asn Tyr Tyr Lys Leu Arg Thr Glu Gly Asp Gly
141          50          55          60
144 Val Tyr Thr Leu Asn Asp Lys Lys Gln Trp Ile Asn Lys Ala Val Gly
145          65          70          75          80
148 Asp Lys Leu Pro Glu Cys Glu Ala Asp Asp Gly Cys Pro Lys Pro Pro
149          85          90          95
152 Glu Ile Ala His Gly Tyr Val Glu His Ser Val Arg Tyr Gln Cys Lys
153          100         105         110
156 Asn Tyr Tyr Lys Leu Arg Thr Glu Gly Asp Gly Val Tyr Thr Leu Asn
157          115         120         125
160 Asn Glu Lys Gln Trp Ile Asn Lys Ala Val Gly Asp Lys Leu Pro Glu
161          130         135         140
164 Cys Glu Ala Val Cys Gly Lys Pro Lys Asn Pro Ala Asn Pro Val Gln
165 145          150          155          160
168 Arg Ile Leu Gly Gly His Leu Asp Ala Lys Gly Ser Phe Pro Trp Gln
169          165          170          175
172 Ala Lys Met Val Ser His His Asn Leu Thr Thr Gly Ala Thr Leu Ile
173          180          185          190

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176 Asn Glu Gln Trp Leu Leu Thr Thr Ala Lys Asn Leu Phe Leu Asn His  
 177 195 200 205  
 180 Ser Glu Asn Ala Thr Ala Lys Asp Ile Ala Pro Thr Leu Thr Leu Tyr  
 181 210 215 220  
 184 Val Gly Lys Lys Gln Leu Val Glu Ile Glu Lys Val Val Leu His Pro  
 185 225 230 235 240  
 188 Asn Tyr Ser Gln Val Asp Ile Gly Leu Ile Lys Leu Lys Gln Lys Val  
 189 245 250 255  
 192 Ser Val Asn Glu Arg Val Met Pro Ile Cys Leu Pro Ser Lys Asp Tyr  
 193 260 265 270  
 196 Ala Glu Val Gly Arg Val Gly Tyr Val Ser Gly Trp Gly Arg Asn Ala  
 197 275 280 285  
 200 Asn Phe Lys Phe Thr Asp His Leu Lys Tyr Val Met Leu Pro Val Ala  
 201 290 295 300  
 204 Asp Gln Asp Gln Cys Ile Arg His Tyr Glu Gly Ser Thr Val Pro Glu  
 205 305 310 315 320  
 208 Lys Lys Thr Pro Lys Ser Pro Val Gly Val Gln Pro Ile Leu Asn Glu  
 209 325 330 335  
 212 His Thr Phe Cys Ala Gly Met Ser Lys Tyr Gln Glu Asp Thr Cys Tyr  
 213 340 345 350  
 216 Gly Asp Ala Gly Ser Ala Phe Ala Val His Asp Leu Glu Glu Asp Thr  
 217 355 360 365  
 220 Trp Tyr Ala Thr Gly Ile Leu Ser Phe Asp Lys Ser Cys Ala Val Ala  
 221 370 375 380  
 224 Glu Tyr Gly Val Tyr Val Lys Val Thr Ser Ile Gln Asp Trp Val Gln  
 225 385 390 395 400  
 228 Lys Thr Ile Ala Glu Asn  
 229 405  
 232 <210> SEQ ID NO: 3  
 233 <211> LENGTH: 347  
 234 <212> TYPE: PRT  
 235 <213> ORGANISM: Ateles geoffroyi  
 237 <400> SEQUENCE: 3  
 239 Met Ser Ala Leu Gly Ala Val Ile Ala Leu Leu Leu Trp Gly Gln Leu  
 240 1 5 10 15  
 243 Phe Ala Val Asp Ser Gly Asn Asp Val Thr Asp Ile Ala Asp Asp Gly  
 244 20 25 30  
 247 Cys Pro Lys Pro Pro Glu Ile Ala Asn Gly Tyr Val Glu His Leu Val  
 248 35 40 45  
 251 Arg Tyr Gln Cys Lys Lys Tyr Tyr Arg Leu Arg Thr Glu Gly Asp Gly  
 252 50 55 60  
 255 Val Tyr Thr Leu Asn Asn Glu Lys Gln Trp Thr Asn Lys Ala Val Gly  
 256 65 70 75 80  
 259 Asp Lys Leu Pro Glu Cys Glu Ala Val Cys Gly Lys Pro Lys Asn Pro  
 260 85 90 95  
 263 Ala Asn Pro Val Gln Arg Ile Leu Gly Gly His Leu Asp Ala Lys Gly  
 264 100 105 110  
 267 Ser Phe Pro Trp Gln Ala Lys Met Val Ser Arg His Asn Leu Thr Thr  
 268 115 120 125

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```

271 Gly Ala Thr Leu Ile Asn Glu Gln Trp Leu Leu Thr Thr Ala Lys Asn
272     130           135           140
275 Leu Phe Leu Asn His Ser Glu Asn Ala Thr Ala Lys Asp Ile Ala Pro
276     145           150           155           160
279 Thr Leu Thr Leu Tyr Val Gly Lys Asn Gln Leu Val Glu Ile Glu Lys
280           165           170           175
283 Val Val Leu Tyr Pro Asn Tyr Ser Gln Val Asp Ile Gly Leu Ile Lys
284           180           185           190
287 Leu Lys Asp Lys Val Pro Val Asn Glu Arg Val Met Pro Ile Cys Leu
288           195           200           205
291 Pro Ser Lys Asp Tyr Ala Glu Val Gly Arg Val Gly Tyr Val Ser Gly
292           210           215           220
295 Trp Gly Arg Asn Ala Asn Phe Lys Phe Thr Asp His Leu Lys Tyr Val
296     225           230           235           240
299 Met Leu Pro Val Ala Asp Gln Tyr Gln Cys Val Lys His Tyr Glu Gly
300           245           250           255
303 Ser Thr Val Pro Glu Lys Lys Thr Pro Lys Ser Pro Val Gly Gln Gln
304           260           265           270
307 Pro Ile Leu Asn Glu His Thr Phe Cys Ala Gly Met Ser Lys Tyr Gln
308           275           280           285
311 Glu Asp Thr Cys Tyr Gly Asp Ala Gly Ser Ala Phe Ala Val His Asp
312           290           295           300
315 Leu Glu Glu Asp Thr Trp Tyr Ala Ala Gly Ile Leu Ser Phe Asp Lys
316     305           310           315           320
319 Ser Cys Gly Val Ala Glu Tyr Gly Val Tyr Val Lys Ala Thr Ser Ile
320           325           330           335
323 Gln Asp Trp Val Gln Lys Thr Ile Ala Glu Asn
324           340           345
327 <210> SEQ ID NO: 4
328 <211> LENGTH: 347
329 <212> TYPE: PRT
330 <213> ORGANISM: Mus caroli
332 <400> SEQUENCE: 4
334 Met Arg Ala Leu Gly Ala Val Val Thr Leu Leu Leu Trp Gly Gln Leu
335     1           5           10           15
338 Phe Ala Val Glu Leu Gly Asn Asp Ala Met Asp Phe Glu Asp Asp Ser
339           20           25           30
342 Cys Pro Lys Pro Pro Glu Ile Ala Asn Gly Tyr Val Glu His Leu Val
343           35           40           45
346 Arg Tyr Arg Cys Arg Gln Phe Tyr Arg Leu Arg Ala Glu Gly Asp Gly
347           50           55           60
350 Val Tyr Thr Leu Asn Asp Glu Lys Gln Trp Met Asn Thr Val Ala Gly
351     65           70           75           80
354 Glu Lys Leu Pro Glu Cys Glu Ala Val Cys Gly Lys Pro Lys His Pro
355           85           90           95
358 Val Asp Gln Val Gln Arg Ile Ile Gly Gly Ser Met Asp Ala Lys Gly
359           100          105          110
362 Ser Phe Pro Trp Gln Ala Lys Met Ile Ser Arg His Gly Leu Thr Thr
363           115          120          125

```

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Input Set : A:\MOESTRUP1A.txt

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366 Gly Ala Thr Leu Ile Ser Asp Gln Trp Leu Leu Thr Thr Ala Lys Asn  
 367 130 135 140  
 370 Leu Phe Leu Asn His Ser Glu Thr Ala Ser Gly Lys Asp Ile Ala Pro  
 371 145 150 155 160  
 374 Thr Leu Thr Leu Tyr Val Gly Lys Asn Gln Leu Val Glu Ile Glu Lys  
 375 165 170 175  
 378 Val Ile Leu His Pro Asn His Ser Val Val Asp Ile Gly Leu Ile Lys  
 379 180 185 190  
 382 Leu Lys Gln Arg Val Leu Val Thr Glu Arg Val Met Pro Ile Cys Leu  
 383 195 200 205  
 386 Pro Ser Lys Asp Tyr Val Ala Pro Gly Arg Val Gly Tyr Val Ser Gly  
 387 210 215 220  
 390 Trp Gly Arg Asn Gln Asp Phe Arg Phe Thr Asp Arg Leu Lys Tyr Val  
 391 225 230 235 240  
 394 Met Leu Pro Val Ala Asp Gln Asp Lys Cys Val Val His Tyr Glu Lys  
 395 245 250 255  
 398 Ser Thr Val Pro Glu Lys Lys Asn Phe Thr Ser Pro Val Gly Val Gln  
 399 260 265 270  
 402 Pro Ile Leu Asn Glu His Thr Phe Cys Ala Gly Leu Thr Lys Tyr Glu  
 403 275 280 285  
 406 Glu Asp Thr Cys Tyr Gly Asp Ala Gly Ser Ala Phe Ala Ile His Asp  
 407 290 295 300  
 410 Met Glu Glu Asp Thr Trp Tyr Ala Ala Gly Ile Leu Ser Phe Asp Lys  
 411 305 310 315 320  
 414 Ser Cys Ala Val Ala Glu Tyr Gly Val Tyr Val Arg Ala Thr Asp Leu  
 415 325 330 335  
 418 Lys Asp Trp Val Gln Glu Thr Met Ala Lys Asn  
 419 340 345  
 422 <210> SEQ ID NO: 5  
 423 <211> LENGTH: 347  
 424 <212> TYPE: PRT  
 425 <213> ORGANISM: Mus musculus  
 427 <400> SEQUENCE: 5  
 429 Met Arg Ala Leu Gly Ala Val Val Thr Leu Leu Leu Trp Gly Gln Leu  
 430 1 5 10 15  
 433 Phe Ala Val Glu Leu Gly Asn Asp Ala Met Asp Phe Glu Asp Asp Ser  
 434 20 25 30  
 437 Cys Pro Lys Pro Pro Glu Ile Ala Asn Gly Tyr Val Glu His Leu Val  
 438 35 40 45  
 441 Arg Tyr Arg Cys Arg Gln Phe Tyr Arg Leu Arg Ala Glu Gly Asp Gly  
 442 50 55 60  
 445 Val Tyr Thr Leu Asn Asp Glu Lys Gln Trp Val Asn Thr Val Ala Gly  
 446 65 70 75 80  
 449 Glu Lys Leu Pro Glu Cys Glu Ala Val Cys Gly Lys Pro Lys His Pro  
 450 85 90 95  
 453 Val Asp Gln Val Gln Arg Ile Ile Gly Gly Ser Met Asp Ala Lys Gly  
 454 100 105 110  
 457 Ser Phe Pro Trp Gln Ala Lys Met Ile Ser Arg His Gly Leu Thr Thr  
 458 115 120 125

Use of n and/or Xaa has been detected in the Sequence Listing.

Review the Sequence Listing to insure a corresponding

explanation is presented in the <220> to <223> fields of

each sequence using n or Xaa.

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/977,577

DATE: 02/08/2002

TIME: 13:59:41

Input Set : A:\MOESTRUP1A.txt

Output Set: N:\CRF3\02082002\I977577.raw

L:606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:2417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21